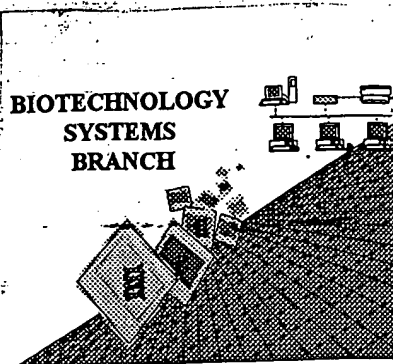


Hollan

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



RECEIVED

SEP 25 2000

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form: TECH CENTER 1600/2900

Application Serial Number: 09/251,133

Source: 1642

Date Processed by STIC: 9/20/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/251,133

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

A. Hoileran

Page 1 of 4

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8 AM

9/27/00

SEP 28 2000

1642

TECH CENTER 1600/2900

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/251,133

DATE: 09/20/2000

TIME: 16:21:27

Input Set : A:\Kumed15

Output Set: N:\CRF3\09202000\I251133.raw

3 <110> APPLICANT: SHAH, Girish V.
5 <120> TITLE OF INVENTION: NEUROENDOCRINE MARKER OF PROSTATE CANCER AND METHOD FOR
6 PRODUCING SAME
8 <130> FILE REFERENCE: 70009590-015
10 <140> CURRENT APPLICATION NUMBER: 09/251,133
11 <141> CURRENT FILING DATE: 1999-02-16
13 <150> PRIOR APPLICATION NUMBER: US 60/074,809
14 <151> PRIOR FILING DATE: 1998-02-17
16 <160> NUMBER OF SEQ ID NOS: 12
18 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

97 <210> SEQ ID NO: 3
98 <211> LENGTH: 433
99 <212> TYPE: DNA
100 <213> ORGANISM: Homo sapien
102 <400> SEQUENCE: 3
103 agaaccctgtg tgcctgggcta cctgcatata gtgccagagt tcatcgaatc tcagctgctg 60
104 gggctcctta gtcctgtttc actttaacca tatgcaagac attcctcaac gttataggca 120
105 agtagactgc atcttttttt ttcttttttt ttcttttttt ttcttttttt ttctggagct 180
106 ggggaccgaa cccaggacct tgcgcttgct aggcgaagcgc tctaccaactg agctaaatcc 240
E--> 107 caaccccgac tgcctgtttt ttggttttta gttaaatcc ggtttgctct atttcgtgt 300
E--> 108 tccctttgtt taaaagaaac tgtagccggg gtagtatatg tctataatcc cagcagttgg 360
E--> 109 gaggcaggag gatccagagt tcaagtcggc atggcacaca tgagacatta gctcaaaaaa 420
E--> 110 aaaaaaaaaa aaa
129 <210> SEQ ID NO: 5
130 <211> LENGTH: 435
131 <212> TYPE: DNA
132 <213> ORGANISM: Homo sapien
134 <400> SEQUENCE: 5
135 attagaacct gtgtgctggg ctacctgcat atagtgccag agttcatcga atctcagctg 60
136 ctggggctcc ttagtctctg ttctttaac catatgcaag acattcctca acgttatagg 120
137 caagtagact gcatcttttt ttcttttttt ttcttttttt ttcttttttt ttcttcggag 180
138 ctgggggaccg aaccaggac cttgcgcttg ctaggcaagc gctctaccac tgagctaaat 240
139 ccccaacccc gactgcatcg tttttggttt ttagttaaat tccggtttgc tctatttcgt 300
E--> 140 gttccctttt gtttaaaaga aactgtagcc ggggtagtat atgtctataa tcccagcagt 360
E--> 141 tgggaggcag gaggatccag agttcaagtc ggcattggcac acatgagaca ttagctcaaa 420
E--> 142 aaaaaaaaaa aaaaa
183 <210> SEQ ID NO: 9
184 <211> LENGTH: 103
185 <212> TYPE: PRT
186 <213> ORGANISM: Homo sapien
188 <400> SEQUENCE: 9
189 Arg Thr Cys Val Leu Gly Tyr Leu His Ile Val Pro Glu Phe Ile Glu
190 1 5 10 15

invalid base (nucleic
designator and)
nos. off, as a result
of above error

invalid
359
numbering off

see next page

RAW SEQUENCE LISTING

DATE: 09/20/2000

PATENT APPLICATION: US/09/251,133

TIME: 16:21:27

Input Set : A:\Kumed15

Output Set: N:\CRF3\09202000\I251133.raw

```

192 Ser Gln Leu Leu Gly Leu Leu Ser Pro Val Ser Phe Asn His Met Gln
193                20                25                30
195 Asp Ile Pro Gln Arg Tyr Arg Gln Val Asp Cys Ile Phe Phe Phe Leu
196                35                40                45
198 Phe Phe Ser Phe Ser Phe Phe Phe Ser Glu Leu Gly Thr Glu Pro
E--> 199      50 50      55      60
201 Arg Thr Leu Arg Leu Leu Gly Lys Arg Ser Thr Thr Glu Leu Asn Pro
E--> 202 65      70 70      75 75      80 80
204 Gln Pro Arg Leu His Arg Phe Trp Phe Leu Val Lys Phe Arg Phe Ala
E--> 205      85 85      90 90      95 95
207 Leu Phe Arg Val Pro Phe Val
E--> 208      100

```

*misaligned
amino acid nos.
(see item 4
on Erra Summary
sheet)*

PTI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 09/20/2000

PATENT APPLICATION: US/09/251,133

TIME: 16:21:28

Input Set : A:\Kumed15

Output Set: N:\CRF3\09202000\I251133.raw

L:87 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:107 M:254 E: No. of Bases conflict, LENGTH:Input:300 Counted:299 SEQ:3
M:254 Repeated in SeqNo=3
L:110 M:252 E: No. of Seq. differs, <211>LENGTH:Input:433 Found:432 SEQ:3
L:140 M:254 E: No. of Bases conflict, LENGTH:Input:360 Counted:359 SEQ:5
L:140 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
M:254 Repeated in SeqNo=5
L:142 M:252 E: No. of Seq. differs, <211>LENGTH:Input:435 Found:434 SEQ:5
L:199 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9